Application No.: 09/646,778

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Raw Sequence Listing Error Summary

ERROR DETECTED | **SUGGESTED CORRECTION** | **SERIAL NUMBER:** 09/646,778

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9 ✓	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

delete
~~Sequenzprotokoll~~

<110> metaGen Gesellschaft f r Genomforschung mbH

<120> Menschliche Nukleins„uresequenzen aus Ovartumorgewebe

use English for a U.S. application

<130> 51580AWOM1XX24-P

<140> PCT/DE99/01087
<141> 1999-04-07

Does Not Comply
Corrected Diskette Needed

<160> 307

<210> 1
<211> 2434
<212> DNA
<213> Homo sapiens

<400> 1

cgggatttta cccggtttaa aaagcgaacc ttctcccggc tacacccgaa ggtacccaaa 60
tatgggtagg tccggttttc caacttggca aacgtatggg gaagcccggg gatggcttcc 120

(see pp. 2-3 for more errors)

<210> 278
<211> 401
<212> PRT
<213> Homo sapiens

(global errors)

The type of errors shown exist throughout the entire Listing. Please check all sequences for similar errors.

<400> 278

per 1.822 of Sequence Rules, insert only one space between amino acids

Met	Pro	Asn	Phe	Cys	Ala	Ala	Pro	Asn	Cys	Thr	Arg	Lys	Ser	Thr	Gln
1				5					10					15	
Ser	Asp	Leu	Ala	Phe	Phe	Arg	Phe	Pro	Arg	Asp	Pro	Ala	Arg	Cys	Gln
			20					25					30		
Lys	Trp	Val	Glu	Asn	Cys	Arg	Arg	Ala	Asp	Leu	Glu	Asp	Lys	Thr	Pro
		35					40					45			
Asp	Gln	Leu	Asn	Lys	His	Tyr	Arg	Leu	Cys	Ala	Lys	His	Phe	Glu	Thr
	50					55					60				
Ser	Met	Ile	Cys	Arg	Thr	Ser	Pro	Tyr	Arg	Thr	Val	Leu	Arg	Asp	Asn
65					70					75					80
Ala	Ile	Pro	Thr	Ile	Phe	Asp	Leu	Thr	Ser	His	Leu	Asn	Asn	Pro	His
				85					90					95	
Ser	Arg	His	Arg	Lys	Arg	Ile	Lys	Glu	Leu	Ser	Glu	Asp	Glu	Ile	Arg
			100					105					110		
Thr	Leu	Lys	Gln	Lys	Lys	Ile	Asp	Glu	Thr	Ser	Glu	Gln	Glu	Gln	Lys
		115					120					125			
His	Lys	Glu	Thr	Asn	Asn	Ser	Asn	Ala	Gln	Asn	Pro	Ser	Glu	Glu	Glu
	130					135					140				
Gly	Glu	Gly	Gln	Asp	Glu	Asp	Ile	Leu	Pro	Leu	Thr	Leu	Glu	Glu	Lys
145					150					155					160
Glu	Asn	Lys	Glu	Tyr	Leu	Lys	Ser	Leu	Phe	Glu	Ile	Leu	Ile	Leu	Met
				165					170					175	
Gly	Lys	Gln	Asn	Ile	Pro	Leu	Asp	Gly	His	Glu	Ala	Asp	Glu	Ile	Pro
			180					185					190		
Glu	Gly	Leu	Phe	Thr	Pro	Asp	Asn	Phe	Gln	Ala	Leu	Leu	Glu	Cys	Arg
		195					200					205			
Ile	Asn	Ser	Gly	Glu	Glu	Val	Leu	Arg	Lys	Arg	Phe	Glu	Thr	Thr	Ala
	210					215					220				
Val	Asn	Thr	Leu	Phe	Cys	Ser	Lys	Thr	Gln	Gln	Arg	Gln	Met	Leu	Glu
225					230					235					240
Ile	Cys	Glu	Ser	Cys	Ile	Arg	Glu	Glu	Thr	Leu	Arg	Glu	Val	Arg	Asp
				245					250					255	
Ser	His	Phe	Phe	Ser	Ile	Ile	Thr	Asp	Asp	Val	Val	Asp	Ile	Ala	Gly
			260					265					270		

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Glu	Glu	His	Leu	Pro	Val	Leu	Val	Arg	Phe	Val	Asp	Glu	Ser	His	Asn
		275					280					285			
Leu	Arg	Glu	Glu	Phe	Ile	Gly	Phe	Leu	Pro	Tyr	Glu	Ala	Asp	Ala	Glu
	290					295					300				
Ile	Leu	Ala	Val	Lys	Phe	His	Thr	Met	Ile	Thr	Glu	Lys	Trp	Gly	Leu
305					310					315					320
Asn	Met	Glu	Tyr	Cys	Arg	Gly	Gln	Ala	Tyr	Ile	Val	Ser	Ser	Gly	Phe
				325					330					335	
Ser	Ser	Lys	Met	Lys	Val	Val	Ala	Ser	Arg	Leu	Leu	Glu	Lys	Tyr	Pro
			340					345					350		
Gln	Ala	Ile	Tyr	Thr	Leu	Cys	Ser	Ser	Cys	Ala	Leu	Asn	Met	Trp	Leu
		355					360					365			
Ala	Lys	Ser	Val	Pro	Val	Met	Gly	Val	Ser	Val	Ala	Leu	Gly	Thr	Ile
	370					375					380				
Glu	Glu	Val	Cys	Ser	Phe	Phe	His	Xxx	Ile	Thr	Thr	Thr	Ala	Phe	Arg
385					390					395					400

Thr

invalid

use Xaa and explain in <220> - <223> sections

see 1.823 d) Sequence Rules and item 9 on Error Summary Sheet

FYI

Use of n or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.